





Figure 5

Sample ID (comment): R4A3F37m1957

Database searched: NCBInr. 7.5.97 Molecular weight search (1000 - 100000 Da) selects 269572 entries. Species search (HOMO SAPIENS) selects 22771 entries.

Combined molecular weight and species scarches select 20933 entries. Number of sequences passing through parent mass filter: 84015 for Types Considered: a b B y n h I

unmodified Hydrogen (II) Free Acid (O II) Scarch Max.# Peptide Masses Digest Max.# Missed Cysteines Peptide Mode Unnatched Ions are Used Cleavages Modified by N terminus identity 5 Par(mi)Frag(av) No enzyme I unmodified Hydrogen (II)

Peptide C terminus

search selects 257 entries.

Parent mass: 1957.2000 (+/- 500.0000 ppm)
Fragment Ions used in search: 175.5, 230.3, 331.5, 387.1, 414.1, 431.7, 442.7, 448.8, 460.8, 533.8, 605.0, 704.2, 1224.8, 1425.5, 1628.6, 1801.4, 1914.9, 1940.8 (+/- 2500.00 ppm)
Composition Ions present: [RPJVINR][KQ]FSDR

Result Summary

	# Unmatched Protein Name Ions	(D82930) III.A-A26 variant	(U25971) MHC class Lantigen 1H.A-A2407	(X82161) HLA-A alpha1 and alpha2 domains	(D32129) III.A-A26	(Z97370) human leukocyte antigen	(U18930) MHC class I antigen HLA-A2	(M16010) III.A-A11 class I antigen (AA at 30)	(AF017310) MHC class I antigen	(AF017309) MHC class Lantigen	(AF012767) MHC class I antigen HLA-A heavy chain
	# Unmated Ions	2	7	2	2	7	7	7	2	2	2
•	Sequence	(Y) <u>VDDTQFVRFDSDAASQR(M)</u>	(Y) <u>VDDTQFVRFDSDAASQR</u> (M)	(Y)VDDTQFVRFDSDAASQR(M)	(Y)VDDTQFVRFDSDAASQR(M)	(Y) <u>VDDTQFVRFDSDAASQR</u> (M)	(Y) <u>VDDTQFVRFDSDAASQR</u> (M)	(Y) <u>VDDTQFVRFDSDAASQR</u> (M)	(Y) <u>VDDTQFVRFDSDAASQR</u> (M)	(Y) <u>VDDTQFVRFDSDAASQR</u> (M)	(Y) <u>VDDTQFVRFDSDAASQR</u> (M)
	Species Calculated MII+ Species MII+ (Da) (Da)	21251.4 HOMO 1956.9052 0.2948 SAPIENS	40679.8 HOMO 1956.9052 0.2948 SAPIENS	20921.2 HOMO 1956.9052 0.2948 SAPIENS	41113.1 HOMO 1956.9052 0.2948	38703.4 HOMO 1956.9052 0.2948 SAPIENS	40895.1 HOMO 1956.9052 0.2948	38355.8 SAPIENS 1956.9052 0.2948	10423.4 HOMO 1956.9052 0.2948	10430.3 HOMO 1956.9052 0.2948	21027.3 HOMO 1956.9052 0.2948 SAPIENS
	Protein MW (Da)	21251.4 ^H	40679.8 ¹¹	20921.2 ¹¹	41113.1 <mark>H</mark>	38703.4 ^H S.	40895.1 S.	38355.8 ¹¹	10423.4 ¹¹ S,	10430.3 ¹¹	21027.3 ¹¹ S,
	NCBlur.7.5.97 Accession#	1839795	915219	825673	994765	2505934	717123	785055	2394324	2394322	2394009
	Rank MS-DigestNCBlnr.7.5.97 Protein index # Accession # (Da)	1 240839	152874	1 141923	1 159176	1 282322	1 133479	1 49436	277806	1 277805	1 277713
	-										

THE LESS SHEET STAND

Figure 5 QDIH223771H22377 ym57e02.rl Homo syptems cOMA clene 52727 5' similar to QD:XO0492 cds1 HLA CLASS 1 HISTOCOMPATIBILITY ANTICEM, A-3 A-0301 ACLWA (HUMINI). LATAN + 4439 <u>9DIAMS486161AS18615</u> (1) 19402.31 HC1_CRAF_ANT Homo suptions celta clone UNABLE 1945 Stinitist to 95(2168) HLA CLASS 1 HISTOCORPATIBILITY ANTICED, A-2. A-0.00; ALPHA (HISTORI); Langth 539 <u>abirlijodinij904</u> y162603.rl Hedd addend odnik otone 26701 5' similar to addendio addendio addiniar dodiniar dodiniar addiniar addiniari addiniar <u>qpinal471511Aaj47151</u> 2032006.r; Stratagene onton (1937201) Rose septens color (1937201) Rose septens color (1937201) Right (1937201) Righ Score - 90 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05 Identities = 19/18 (1001), Positives = 18/18 (1001), Frame - -1 Score = 90 (41.9 bits), Expect = 9.1m-65, P = 8.1m-01 Identities = 18/19 (1001), Positions = 18/19 (1001), Fines = +1 Score + 30 (41.9 bita), Expect = 0.16-35, P = 0.18-05 Identities = 11/18 (1004), Posttives = 18/18 (1001), Frame = +2 Score = 30 (41.3 bits), Expans = 8.(e=05, F = 8.te=05 [dontities = 12/18 (1004), Positives = 19/18 (1004), Frame Ouery: I VDDTSFYREDSDAAGOR: 19 VDDTQFYREDSDAAGOR: Sbjor: 152 VEDTGFYREDSDAASOR: 205 Overy: | VCDTOFVRFDSDAASGR: 18 VCDTOFVRFDSBAASGRE SBJCL: 154 VCDTOFVRFDSDAASGRE 207 Ouery: | VEDIOFYREDSDAAGOPH 18 VEDIGFYREDSHAAGOPH SDJCt: | 116 VEDIOFYREDSHAAGOPH 1999 L VEDTGEVREDSDAASOR: 18 VESTOFVREDSDAASOR: 13 VEDTGEVREDSDAASOR: 66 Plus Strand HSF4: Plus Strand HSPs: Plus Strand MSPs: Plus Strand HSFs: Sbjet: Overy <u>gbini20déini20de</u> yf?idio.ri Homo sapiens com clong 26062 5' stailar to Ter:00472, casi HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-3 A-0301 Lentth' - 405 <u>qbins97641A19764</u> yhd7c35.ct Hosm sapiens coud clone 42563 5' steilist to 70:700492 cdst HLA CLASS I HISTOCKHPATIBILITY AHTIGEB, A-3 A-0301 APA (HPSAH). <u>4bladd893alaad893al</u> 4b37f09.cl Steatagent Hela cell sl 917216 Homo 846:Am - 501A clone 813015 S' similar to jo:LOG425 HLA CLASS I HISTOCHATIBILITY ANTIOCH. 84-344a-101 A-3402 ALPHA (HUHAM); Lensth - 479 QDIAN1326331AN123553 ro21a05.c1 Stratagen colon (*137704) Homo septens CHG CTON 53704 5' stmilar to 3b124663) HLA CLASS t HISTOCKHARIBILITY ANTICEN, A-2 A-0201 ALPHA (HUMAN); Entry h * 4.29 Score - 90 (41,7 bits), Expect - 9.1e-05, P = 9.1e-05 Identities - 13/19 (1901), Positives - 18/18 (1901), Frame - +2 Score = 90 (41.9 bits), Expect = 3.1e-05, P = 5.1e-05 Identities = 13/18 (1001), Positives = 19/18 (1001), Frame = +3 Score + 70 141.9 bits), Expect - 1.14-55, P - 6.14-55 Identities - 13/18 (1001), Fositions - 13/18 (1001), Frame + +1 Score - 90 (41.9 bits), Espect - 4.1e-75, P - 8.1e-75 Identities - 18/18 (1001), fositives - 18/18 (1001), frame - 13 Ouery: I VDCTOFYREDSDAASOR! 18 VDDTOFVREDSDAASOR! Sbjet: 154 VDDTOFYRFOSDAASOP! 211 Query: 1 VD370F/RFDSDANSQFH 18 VDD10FVRFDSDANSQFH Sbjet: 150 VD070FVRFDSDANSQRH 203 Query: 1 VCDTOFVREDSDAASORH 18 VCDTOFVREDSCAASORH Sbjet: 157 VDDTOFVREDSDAASQEH 210 Ouery: 1 VOCTOFTPEDSDAASOR: 19 VOOTGEVETSSCAASOR: Sbjot: 138 VOCTGEVEDSCAASOR: 191 Plus Strand RSFs: Plus Strand HSPs: Plus Strand HSPs: Plus Strand 4SPs:

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